

## APPENDIX A

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#
# Aligned_sequences: 2
# 1: Yoshinaga_2
# 2: Ling_7
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 316
# Identity:      112/316 (35.4%)
# Similarity:    112/316 (35.4%)
# Gaps:          204/316 (64.6%)
# Score: 566.0
#
#=====

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Yoshinaga_2	1	MLRRRGSPGMGVHGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCC	50
Ling_7	1	ALEVQVPEDPVVALVGTDATLCC	23
Yoshinaga_2	51	SFSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLL	100
Ling_7	24	SFSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLL	73
Yoshinaga_2	101	AQGNASLRLQRVRVADEGSFTCFVSIIRDFGSAAVSLQVAAPYSKPSMTLE	150
Ling_7	74	AQGNASLRLQRVRVADEGSFTCFVSIIRDFGSAAVSLQVA	112
Yoshinaga_2	151	PNKDLRPGDITVTITCSSYRGYPEAEVFWQDGGVPLTGNVTTSQMANEQG	200
Ling_7	113		112
Yoshinaga_2	201	LFDVHVSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTTITGQPMTFPPEALW	250
Ling_7	113		112
Yoshinaga_2	251	VTVGLSVCLIALLVALAFVCWRKIKQSCEENAGAEDQDGELEGSKTALQ	300
Ling_7	113		112
Yoshinaga_2	301	PLKHSKSKEDDGQEIA	316
Ling_7	113		112